

SEQUENCE LISTING

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<110> WANG, Bryan S.
      PABO, Carl O.
<120> DIMERIZING PEPTIDES
<130> 8325-1004 / M4-US1
<140> 09/636,243
<141> 2000-08-10
<150> 60/148,422
<151> 1999-08-11
<160> 83
<170> PatentIn Ver. 2.0
<210> 1
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      motif characterizing C2H2 class proteins
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<223> where Xaa is any amino acid
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Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
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Xaa Xaa His Xaa Xaa Xaa Xaa His

20 25

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<210> 2
<211> 4
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<213> Artificial Sequence
<223> Description of Artificial Sequence: D-able subsite
<220>
<221> misc_feature
<222> (1)..(2)
<223> n = a, t, g or c
<220>
<221> misc_feature
<222> (4)
<223> k = g or t
<400> 2
nngk
                                                                    4
<210> 3
<211> 9
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      protein bind sequence
<400> 3
                                                                    9
ggcgtagac
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<223> Description of Artificial Sequence: zinc finger
      protein bind sequence
<400> 4
ggcgacgta
                                                                    9
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<400> 5
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Thr Gly Glu Lys Pro
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Gly Gly Gly Ser
<210> 7
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Gly Gly Arg Arg Gly Gly Ser
<210> 8
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Leu Arg Gln Arg Asp Gly Glu Arg Pro
<210> 9
<211> 12
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Leu Arg Gln Lys Asp Gly Gly Gly Ser Glu Arg Pro
<210> 10
<211> 16
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<210> 11
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     finger of zinc finger protein
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<221> SITE
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Xaa Xaa His Xaa Xaa Xaa Xaa His
            20
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      domain Fl
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Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser Asp
Glu Leu Thr Arg His Ile Arg Ile His Thr Gly Gln Lys Pro
<210> 13
<211> 28
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      domain F2
<400> 13
Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp His Leu
Thr Thr His Ile Arg Thr His Thr Gly Glu Lys Pro
<210> 14
<211> 38
<212> DNA
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     site
ggttgcagtg ggcgcgccca cagtacttga acgtaacg
                                                                   38
<210> 15
<211> 34
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: DNA binding
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cgttacgttc aagtactgtg ggcgcgccca ctgc
                                                                   34
<210> 16
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<213> Artificial Sequence

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tgggcgtatg ct
                                                                    12
<210> 17
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agcatacgcc ca
                                                                   12
<210> 18
<211> 57
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      site
ggaattcctg atcaagatct ggtcacgtcc ataggctagg catgtcaagg ctgtatg
                                                                   57
<210> 19
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gggatccact cgcgaacgcg tccttgtagt gggcgcgccc acatacaqcc ttqacat
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<212> DNA
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      repeat site
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tgggcgcgcc ca
                                                                   12
<210> 21
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<223> Description of Artificial Sequence:
      self-complementary oligonucleotide
<400> 21
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atgggcgcgc ccat
<210> 22
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<223> Description of Artificial Sequence: peptide
      extension
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<221> SITE
<222> (1)
<223> "His" is numbered 89
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<222> (15)
<223> "Arg" is numbered 103
His Pro Met Asn Asn Leu Leu Asn Tyr Val Val Pro Lys Met Arg
  1
                 5
                                     10
<210> 23
<211> 34
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: DNA site used
      for affinity selection
gcagtgggcg cgcccacagt acttgaacgt aacg
                                                                   34
<210> 24
<211> 15
<212> PRT
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<400> 24
Gly Gly Gln Trp Leu Gly Thr Trp Glu Trp Tyr Gly Pro Lys
                                     10
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<211> 15
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<223> Description of Artificial Sequence: peptide 2
<400> 25
Tyr Glu Lys Ile Ser Val Glu Gly Ile Lys Asp Val Arg Val Arg
<210> 26
<211> 15
<212> PRT
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<400> 26
Asn Val Ser Ile Glu Gly Val Leu Lys Tyr Tyr Arg Gly Leu Arg
                                     10
<210> 27
<211> 15
<212> PRT
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Arg Ser Cys Gly Leu Asp Tyr Glu Gly Tyr Trp Leu Lys Leu Lys
                 5
<210> 28
<211> 15
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<223> Description of Artificial Sequence: peptide 5
<400> 28
Ser Arg Trp Leu Glu Glu Glu Val Ser Arg Leu Leu Leu Arg
<210> 29
<211> 15
<212> PRT
<213> Artificial Sequence
<220>
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<400> 29
Gly Glu Ala Leu Asp Arg Phe Glu Arg Glu Met Lys Leu Met Arg
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Gly Gly Gln Trp
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His Pro Met Asn Asn
  1
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Pro Pro Ser Thr Glu
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Gln Lys Tyr Gly Asp
<210> 34
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Glu Asn Tyr Glu Lys
  1
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Leu Gly Thr Trp Glu
  1
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Leu Leu Asn Tyr Lys
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<211> 5
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Leu Leu Asn Tyr Val
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Leu Leu Asp Tyr Ile
  1
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Leu Leu Asn Tyr Ile
  1
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Leu Leu Gln Tyr Val
  1
                  5
<210> 41
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Leu Leu Glu Tyr Lys
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Leu Leu Asp Tyr Val
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<211> 5
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Leu Leu Asn Tyr Val
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<210> 44
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Trp Tyr Gly Pro Lys
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His Pro Lys Met Lys
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<211> 5
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Pro Ala Lys Ile Arg
  1
<210> 47
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Val Pro Lys Ser Arg
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<210> 48
<211> 5
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Val Pro Arg Leu Lys
 1
<210> 49
<211> 5
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Ala Pro Lys Leu Arg
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<210> 50
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His Ala Lys Ile Arg
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Val Val Lys Met Arg
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Pro Val Lys Met Arg
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Val Pro Lys Gln Arg
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block reoptimization sequence

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Val Pro Lys Met Arg
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Val Arg Lys Leu Arg
 1
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Ser Arg Trp Leu Glu
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<210> 57
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Phe Arg Trp Leu Glu
                  5
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Gln Pro Trp Leu Thr
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<211> 5
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Pro Pro Trp Leu Ile
 1
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Pro Pro Trp Leu Lys
  1
<210> 61
<211> 5
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Pro Ala Trp Leu Thr
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<211> 5
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Pro Ala Trp Leu Ala
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<211> 5
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Trp Ala Trp Leu Asp
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Pro Thr Trp Leu Thr
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Glu Glu Val Ser Arg
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<210> 66
<211> 5
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Glu Tyr Leu Glu Ser
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Asp Tyr Val Thr Gln
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Asp Tyr Leu Ala Asp
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Glu Tyr Leu Thr Phe
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Gln Tyr Leu Glu Asp
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Ser Tyr Leu Asp Lys
  1
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Glu Tyr Met Ser Asp
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Leu Leu Leu Arg
<210> 75
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Met Arg Leu Trp Arg
<210> 76
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Met Arg Gly Trp Lys
  1
<210> 77
<211> 5
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Met Arg Lys Trp Arg
<210> 78
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Met Arg Lys Trp Lys
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block reoptimization sequence

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Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser

Asp Glu Leu Thr Arg His Ile Arg Ile His 'Thr

<210> 81 <211> 28

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: GLI1

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Glu Thr Asp Cys Arg Trp Asp Gly Cys Ser Gln Glu Phe Asp Ser Gln

Glu Gln Leu Val His His Ile Asn Ser Glu His Ile 20

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<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: GLI2

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Glu Phe Val Cys His Trp Gly Gly Cys Ser Arg Glu Leu Arg Pro Phe

Lys Ala Gln Tyr Met Leu Val Val His Met Arg Arg His Thr 20 25

<210> 83

<211> 27

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: SWI5

<400> 83

Thr Phe Glu Cys Leu Phe Pro Gly Cys Thr Lys Thr Phe Lys Arg Arg 1 5 10 15

Tyr Asn Ile Arg Ser His Ile Gln Thr His Leu 20 25